



IFW16

RAW SEQUENCE LISTING

DATE: 08/11/2004

PATENT APPLICATION: US/09/674,337B

TIME: 16:45:31

Input Set : A:\71555107.app

Output Set: N:\CRF4\08112004\I674337B.raw

3 <110> APPLICANT: MORI, SATOSHI
 4 HIGUCHI, KYOKO
 5 SUZUKI, KAZUYA
 6 NISHIZAWA, NAOKO
 7 NAKANISHI, HIROMI
 9 <120> TITLE OF INVENTION: NICOTIANAMINE SYNTHASE AND GENE ENCODING THE SAME
 11 <130> FILE REFERENCE: 71526-55107
 13 <140> CURRENT APPLICATION NUMBER: 09/674,337B
 14 <141> CURRENT FILING DATE: 2001-07-26
 16 <150> PRIOR APPLICATION NUMBER: PCT/JP99/02305
 17 <151> PRIOR FILING DATE: 1999-04-30
 19 <150> PRIOR APPLICATION NUMBER: JP 10-137685
 20 <151> PRIOR FILING DATE: 1998-04-30
 22 <160> NUMBER OF SEQ ID NOS: 37
 24 <170> SOFTWARE: PatentIn Ver. 3.2
 26 <210> SEQ ID NO: 1
 27 <211> LENGTH: 328
 28 <212> TYPE: PRT
 29 <213> ORGANISM: Hordeum vulgare
 31 <400> SEQUENCE: 1
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 35 Gly Ile Gln Ala Ala Ile Ala Glu Leu Pro Ser Leu Ser Pro Ser Pro
 36 20 25 30
 38 Glu Val Asp Arg Leu Phe Thr Asp Leu Val Thr Ala Cys Val Pro Pro
 39 35 40 45
 41 Ser Pro Val Asp Val Thr Lys Leu Ser Pro Glu His Gln Arg Met Arg
 42 50 55 60
 44 Glu Ala Leu Ile Arg Leu Cys Ser Ala Ala Glu Gly Lys Leu Glu Ala
 45 65 70 75 80
 47 His Tyr Ala Asp Leu Leu Ala Thr Phe Asp Asn Pro Leu Asp His Leu
 48 85 90 95
 50 Gly Leu Phe Pro Tyr Tyr Ser Asn Tyr Val Asn Leu Ser Arg Leu Glu
 51 100 105 110
 53 Tyr Glu Leu Leu Ala Arg His Val Pro Gly Ile Ala Pro Ala Arg Val
 54 115 120 125
 56 Ala Phe Val Gly Ser Gly Pro Leu Pro Phe Ser Ser Leu Val Leu Ala
 57 130 135 140
 59 Ala His His Leu Pro Glu Thr Gln Phe Asp Asn Tyr Asp Leu Cys Gly
 60 145 150 155 160
 62 Ala Ala Asn Glu Arg Ala Arg Lys Leu Phe Gly Ala Thr Ala Asp Gly
 63 165 170 175
 65 Val Gly Ala Arg Met Ser Phe His Thr Ala Asp Val Ala Asp Leu Thr



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66          180          185          190
68 Gln Glu Leu Gly Ala Tyr Asp Val Val Phe Leu Ala Ala Leu Val Gly
69          195          200          205
71 Met Ala Ala Glu Glu Lys Ala Lys Val Ile Ala His Leu Gly Ala His
72          210          215          220
74 Met Val Glu Gly Ala Ser Leu Val Val Arg Ser Ala Arg Pro Arg Gly
75 225          230          235          240
77 Phe Leu Tyr Pro Ile Val Asp Pro Glu Asp Ile Arg Arg Gly Gly Phe
78          245          250          255
80 Glu Val Leu Ala Val His His Pro Glu Gly Glu Val Ile Asn Ser Val
81          260          265          270
83 Ile Val Ala Arg Lys Ala Val Glu Ala Gln Leu Ser Gly Pro Gln Asn
84          275          280          285
86 Gly Asp Ala His Ala Arg Gly Ala Val Pro Leu Val Ser Pro Pro Cys
87          290          295          300
89 Asn Phe Ser Thr Lys Met Glu Ala Ser Ala Leu Glu Lys Ser Glu Glu
90 305          310          315          320
92 Leu Thr Ala Lys Glu Leu Ala Phe
93          325
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98 <212> TYPE: DNA
99 <213> ORGANISM: Hordeum vulgare
101 <220> FEATURE:
102 <221> NAME/KEY: CDS
103 <222> LOCATION: (55)..(1041)
105 <400> SEQUENCE: 2
106 gcgttcagag gcttccagag ttcttcggt caccaagaag catttgatca taac atg 57
107                                     Met
108                                     1
110 gat gcc cag aac aag gag gtc gct gct ctg atc gag aag atc gcc ggt 105
111 Asp Ala Gln Asn Lys Glu Val Ala Ala Leu Ile Glu Lys Ile Ala Gly
112          5          10          15
114 atc cag gcc gcc atc gcc gag ctg ccg tcg ctg agc ccg tcc ccc gag 153
115 Ile Gln Ala Ala Ile Ala Glu Leu Pro Ser Leu Ser Pro Ser Pro Glu
116          20          25          30
118 gtc gac agg ctc ttc acc gac ctc gtc acg gcc tgc gtc ccg ccg agc 201
119 Val Asp Arg Leu Phe Thr Asp Leu Val Thr Ala Cys Val Pro Pro Ser
120          35          40          45
122 ccc gtc gac gtg acg aag ctc agc ccg gag cac cag agg atg cgg gag 249
123 Pro Val Asp Val Thr Lys Leu Ser Pro Glu His Gln Arg Met Arg Glu
124 50          55          60          65
126 gct ctc atc cgc ttg tgc tcc gcc gcc gag ggg aag ctc gag gcg cac 297
127 Ala Leu Ile Arg Leu Cys Ser Ala Ala Glu Gly Lys Leu Glu Ala His
128          70          75          80
130 tac gcc gac ctg ctc gcc acc ttc gac aac ccg ctc gac cac ctc ggc 345
131 Tyr Ala Asp Leu Leu Ala Thr Phe Asp Asn Pro Leu Asp His Leu Gly
132          85          90          95
134 ctc ttc ccg tac tac agc aac tac gtc aac ctc agc agg ctg gag tac 393

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135 Leu Phe Pro Tyr Tyr Ser Asn Tyr Val Asn Leu Ser Arg Leu Glu Tyr
136          100          105          110
138 gag ctc ctg gcg cgc cac gtg ccg ggc atc gcg ccg gcg cgc gtc gcc 441
139 Glu Leu Leu Ala Arg His Val Pro Gly Ile Ala Pro Ala Arg Val Ala
140      115          120          125
142 ttc gtc ggc tcc ggc ccg ctg ccg ttc agc tcg ctc gtc ctc gcc gcg 489
143 Phe Val Gly Ser Gly Pro Leu Pro Phe Ser Ser Leu Val Leu Ala Ala
144 130          135          140          145
146 cac cac ctg ccc gag acc cag ttc gac aac tac gac ctg tgc ggc gcg 537
147 His His Leu Pro Glu Thr Gln Phe Asp Asn Tyr Asp Leu Cys Gly Ala
148          150          155          160
150 gcc aac gag cgc gcc agg aag ctg ttc ggc gcg acg gcg gac gcc gtc 585
151 Ala Asn Glu Arg Ala Arg Lys Leu Phe Gly Ala Thr Ala Asp Gly Val
152          165          170          175
154 ggc gcg cgt atg tcg ttc cac acg gcg gac gtc gcc gac ctc acc cag 633
155 Gly Ala Arg Met Ser Phe His Thr Ala Asp Val Ala Asp Leu Thr Gln
156      180          185          190
158 gag ctc ggc gcc tac gac gtg gtc ttc ctc gcc gcg ctc gtc gcc atg 681
159 Glu Leu Gly Ala Tyr Asp Val Val Phe Leu Ala Ala Leu Val Gly Met
160      195          200          205
162 gca gcc gag gag aag gcc aag gtg att gcc cac ctg ggc gcg cac atg 729
163 Ala Ala Glu Glu Lys Ala Lys Val Ile Ala His Leu Gly Ala His Met
164 210          215          220          225
166 gtg gag ggg gcg tcc ctg gtc gtg ccg agc gca ccg ccc cgc gcc ttt 777
167 Val Glu Gly Ala Ser Leu Val Val Arg Ser Ala Arg Pro Arg Gly Phe
168          230          235          240
170 ctt tac ccc att gtc gac ccg gag gac atc agg ccg ggt ggg ttc gag 825
171 Leu Tyr Pro Ile Val Asp Pro Glu Asp Ile Arg Arg Gly Gly Phe Glu
172          245          250          255
174 gtg ctg gcc gtg cac cac ccg gaa ggt gag gtg atc aac tct gtc atc 873
175 Val Leu Ala Val His His Pro Glu Gly Glu Val Ile Asn Ser Val Ile
176      260          265          270
178 gtc gcc cgt aag gcc gtc gaa gcg cag ctc agt ggg ccg cag aac gga 921
179 Val Ala Arg Lys Ala Val Glu Ala Gln Leu Ser Gly Pro Gln Asn Gly
180      275          280          285
182 gac gcg cac gca ccg ggc gcg gtg ccg ttg gtc agc ccg cca tgc aac 969
183 Asp Ala His Ala Arg Gly Ala Val Pro Leu Val Ser Pro Pro Cys Asn
184 290          295          300          305
186 ttc tcc acc aag atg gag gcg agc gcg ctt gag aag agc gag gag ctg 1017
187 Phe Ser Thr Lys Met Glu Ala Ser Ala Leu Glu Lys Ser Glu Glu Leu
188          310          315          320
190 acc gcc aaa gag ctg gcc ttt tga ttgaagagtgcgcgtgggtca ttctgtcgcc 1071
191 Thr Ala Lys Glu Leu Ala Phe
192          325
194 tgcgacgtg gtaactttcc tactcgtgtg tgttttgatg tttgtgcctg taagagttat 1131
196 gcttccggcc ttgtgctgtt aatttacacg cgttacatgt agtacttgta tttataacctg 1191
198 gaataacggt atgtaacata aatattagtgcgatttgaag tgtaatgcta aataataaga 1251
200 aaacttgatg cagacattca aaaaaaaaaa aaaaaaaaaa aaaa 1295
204 <210>. SEQ ID NO: 3

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Output Set: N:\CRF4\08112004\I674337B.raw

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205 <211> LENGTH: 335
206 <212> TYPE: PRT
207 <213> ORGANISM: Hordeum vulgare
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213 Thr Gly Leu His Ala Ala Ile Ala Lys Leu Pro Ser Leu Ser Pro Ser
214           20           25           30
216 Pro Asp Val Asp Ala Leu Phe Thr Glu Leu Val Thr Ala Cys Val Pro
217           35           40           45
219 Pro Ser Pro Val Asp Val Thr Lys Leu Gly Pro Glu Ala Gln Glu Met
220           50           55           60
222 Arg Glu Gly Leu Ile Arg Leu Cys Ser Glu Ala Glu Gly Lys Leu Glu
223   65           70           75           80
225 Ala His Tyr Ser Asp Met Leu Ala Ala Phe Asp Lys Pro Leu Asp His
226           85           90           95
228 Leu Gly Met Phe Pro Tyr Tyr Asn Asn Tyr Ile Asn Leu Ser Lys Leu
229           100          105          110
231 Glu Tyr Glu Leu Leu Ala Arg Tyr Val Pro Gly Gly Tyr Arg Pro Ala
232           115          120          125
234 Arg Val Ala Phe Ile Gly Ser Gly Pro Leu Pro Phe Ser Ser Phe Val
235           130          135          140
237 Leu Ala Ala Arg His Leu Pro Asp Thr Met Phe Asp Asn Tyr Asp Leu
238   145          150          155          160
240 Cys Gly Ala Ala Asn Asp Arg Ala Ser Lys Leu Phe Arg Ala Asp Arg
241           165          170          175
243 Asp Val Gly Ala Arg Met Ser Phe His Thr Ala Asp Val Ala Asp Leu
244           180          185          190
246 Ala Gly Glu Leu Ala Lys Tyr Asp Val Val Phe Leu Ala Ala Leu Val
247           195          200          205
249 Gly Met Ala Ala Glu Asp Lys Ala Lys Val Ile Ala His Leu Gly Ala
250           210          215          220
252 His Met Ala Asp Gly Ala Ala Leu Val Val Arg Ser Ala His Gly Ala
253   225          230          235          240
255 Arg Gly Phe Leu Tyr Pro Ile Val Asp Pro Gln Asp Ile Gly Arg Gly
256           245          250          255
258 Gly Phe Glu Val Leu Ala Val Cys His Pro Asp Asp Asp Val Val Asn
259           260          265          270
261 Ser Val Ile Ile Ala Gln Lys Ser Lys Asp Val His Ala Asp Gly Leu
262           275          280          285
264 Gly Ser Gly Arg Gly Ala Gly Gly Gln Tyr Ala Arg Gly Thr Val Pro
265           290          295          300
267 Val Val Ser Pro Pro Cys Arg Phe Gly Glu Met Val Ala Asp Val Thr
268   305          310          315          320
270 Gln Asn His Lys Arg Asp Glu Phe Ala Asn Ala Glu Val Ala Phe
271           325          330          335
274 <210> SEQ ID NO: 4
275 <211> LENGTH: 1342
276 <212> TYPE: DNA

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277 <213> ORGANISM: Hordeum vulgare
279 <400> SEQUENCE: 4
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281 gaggtggatg ccctggtgga gaagatcacc gggtcccatg ccgcaatcgc caagctgccg 120
282 tcgtcagcc catccccgga cgtcgacgcg ctcttcacgg agctggtcac ggcgtgcgtt 180
283 ccaccgagtc cagtggacgt gaccaagctc gggccggagg cgcaggagat ggcggagggc 240
284 ctcatccgcc tatgtccga ggcgaggggg aagctggagg cgcactactc cgacatgctc 300
285 gccgccttcg acaagccgct ggatcacctc ggcatgttcc cctactacaa caactacatc 360
286 aacctcagca agctcgagta cgagtcctcg gcccgtacg tgcttgccgg ctatcgcccg 420
287 gcgcgcgtcg cgttcacgg ctccggcccg ctgcccgtca gctcctttgt cctggccgcg 480
288 cgccacctgc ccgacacat gttecgacaac tatgacctgt gcggtgcggc caacgatcgc 540
289 gccagcaagc tcttcgcgc ggatcgcgac gtgggtgcc gcattgcgtt ccacacggcc 600
290 gacgtcgcg accctgcgg cgagtcgcc aagtacgac ttgtcttctt ggcgcactc 660
291 gtcggcatgg ccgcccagga caaggcgaag gtgatcgcg acctcggcgc acacatggca 720
292 gacggggcgc cctcgtcgt gcgcagcgca cacggagcgc gcgggttctt gtaccgatc 780
293 gtcgacccc aggacatcgg ccgaggcggg ttcgaggtgc tggcgtgtg ccatcccgac 840
294 gacgacgtgg tgaactccg catcatcgca cagaagtcca aggacgtgca tgccgatgga 900
295 cttggcagcg ggcgtggtgc cgggtggacag tacgcgcggg gcacggtgcc tgttgtcagc 960
296 ccccggtgca ggttcggcga gatggtggcg gacgtgacct agaaccacaa gagagacgag 1020
297 tttgccaacg ccgaagtggc cttttgatcg ttcgctgcga ggggtgtgat ccatgatcca 1080
298 tccatacctc gttctgtgat tgcacaaac ttgcaatcgt atgcatttca agtcacgtgt 1140
299 tgcttctatc caataatgta cgtgtggtgt ttacacgcga atgtcttgta gacctttgta 1200
300 tgtgtacaag tgaattttaa ttcacaagta catataatgg tcaccattga aaagatgttt 1260
301 agtgtgtgtt ttccaatata tgtttgtgta aggttcatca tctaataaaa tatgtttgga 1320
302 acccaaaaaa aaaaaaaaaa aa 1342
305 <210> SEQ ID NO: 5
306 <211> LENGTH: 335
307 <212> TYPE: PRT
308 <213> ORGANISM: Hordeum vulgare
310 <400> SEQUENCE: 5
311 Met Ala Ala Gln Asn Asn Asn Lys Asp Val Ala Ala Leu Val Glu Lys
312 1 5 10 15
314 Ile Thr Gly Leu His Ala Ala Ile Ala Lys Leu Pro Ser Leu Ser Pro
315 20 25 30
317 Ser Pro Asp Val Asp Ala Leu Phe Thr Glu Leu Val Thr Ala Cys Val
318 35 40 45
320 Pro Pro Ser Pro Val Asp Val Thr Lys Leu Gly Pro Glu Ala Gln Glu
321 50 55 60
323 Met Arg Glu Gly Leu Ile Arg Leu Cys Ser Glu Ala Glu Gly Lys Leu
324 65 70 75 80
326 Glu Ala His Tyr Ser Asp Met Leu Ala Ala Phe Asp Asn Pro Leu Asp
327 85 90 95
329 His Leu Gly Ile Phe Pro Tyr Tyr Ser Asn Tyr Ile Asn Leu Ser Lys
330 100 105 110
332 Leu Glu Tyr Glu Leu Leu Ala Arg Tyr Val Arg Arg His Arg Pro Ala
333 115 120 125
335 Arg Val Ala Phe Ile Gly Ser Gly Pro Leu Pro Phe Ser Ser Phe Val
336 130 135 140
338 Leu Ala Ala Arg His Leu Pro Asp Thr Met Phe Asp Asn Tyr Asp Leu

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RAW SEQUENCE LISTING ERROR SUMMARY
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Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:14; N Pos. 8
Seq#:23; Xaa Pos. 3,9,16,19,24
Seq#:24; Xaa Pos. 7,11
Seq#:25; Xaa Pos. 7
Seq#:26; Xaa Pos. 4
Seq#:28; Xaa Pos. 5,10
Seq#:29; Xaa Pos. 1,2,3,4,5,6,7,8,9,10,12,13,16,17,18,19,20,21,23,24,26,27
Seq#:29; Xaa Pos. 29,31,32,33,34,35,36,39,40,43,44,46,48,49,50,51,54,55,56
Seq#:29; Xaa Pos. 57,58,59,60,62,65,66,69,70,72,73,76,77,80,82,83,84,85,87
Seq#:29; Xaa Pos. 88,89,91,94,97,98,102,103,106,107,109,110,113,114,117,118
Seq#:29; Xaa Pos. 119,120,121,122,123,124,125,126,127,128,131,138,139,141
Seq#:29; Xaa Pos. 142,145,146,149,150,151,152,154,156,157,158,159,160,161
Seq#:29; Xaa Pos. 164,165,167,168,170,171,172,173,174,175,176,177,178,179
Seq#:29; Xaa Pos. 182,184,186,187,188,189,190,191,192,193,194,196,197,198
Seq#:29; Xaa Pos. 206,210,211,212,213,215,216,217,218,219,222,223,226,227
Seq#:29; Xaa Pos. 230,232,233,234,235,236,237,238,240,245,247,248,249,250
Seq#:29; Xaa Pos. 251,252,253,254,257,260,262,265,266,267,269,272,273,274
Seq#:29; Xaa Pos. 275,276,278,279,280,281,282,283,284,285,286,287,288,289
Seq#:29; Xaa Pos. 290,291,292,293,294,295,296,297,298,299,300,301,302,303
Seq#:29; Xaa Pos. 304,305,306,307,308,309,310,311,312,313,314,315,316,317
Seq#:29; Xaa Pos. 318,319,320,321,322,323,324,325,326,327,328

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Input Set : A:\71555107.app

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L:1214 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:23 after pos.:0
M:341 Repeated in SeqNo=23
L:1242 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:24 after pos.:0
L:1261 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:25 after pos.:0
L:1280 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:26 after pos.:0
L:1318 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:28 after pos.:0
L:1627 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:29 after pos.:0
M:341 Repeated in SeqNo=29